

AMENDMENTS

Amendments to the Specification:

At page 32, beginning at line 19, insert the following replacement paragraphs:

FIG. 2A. Shown is the nucleotide and predicted amino acid sequence of sentrin-1 cDNA (SEQ ID NOS:17 and 18). Nucleotides are numbered on the left and amino acid residues are numbered on the right. The start codon ATG and the stop codon TAG are single underlined. Amino acids are indicated in the single letter code.

FIG. 2B. Shown is the homology of sentrin-1 and ubiquitin (SEQ ID NOS:2, 13, 14, 15, and 16). A BLAST search of the entire data base through the National Center for Biotechnology Information (Bethesda, MD) (Altschul *et al.*, 1990) revealed sequence homology of sentrin-1 with the yeast *Saccharomyces cerevisiae* Smt3, ubiquitin, Nedd8, the ubiquitin domain to Bag-1 (37-73). Residues identical between sentrin-1 and Smt3 are shown in bold; Residues identical among all sequences are shaded.

At page 35, beginning at line 13, insert the following replacement paragraph:

FIG. 12. Amino acid alignment of NEDD8, ubiquitin, and the sentrin family members. Identical amino acids are printed in bold type (SEQ ID NOS:2, 4, 6, 14 and 15). Lys48 of ubiquitin, critical for the formation of ubiquitin multimers, is indicated by an open triangle. The Gly residue critical for conjugation is marked by a closed triangle. Accession numbers for human NEDD8, sentrin-1 (DNA: SEQ ID NO:1; protein: SEQ ID NO:2), sentrin-2 (DNA: SEQ ID NO:3; protein, SEQ ID NO:4), and sentrin-3 (DNA: SEQ ID NO:5; protein, SEQ ID NO:6) are D23662/AA484409/N24312, U83117, X99585/T08096 and X99584, respectively.

Please delete the Sequence Listing numbered pages 1 through 6 and insert therefor the 8 page Substitute Sequence Listing attached as Appendix A.